The Genetics of Carbon Allocation and Partitioning in *Populus*

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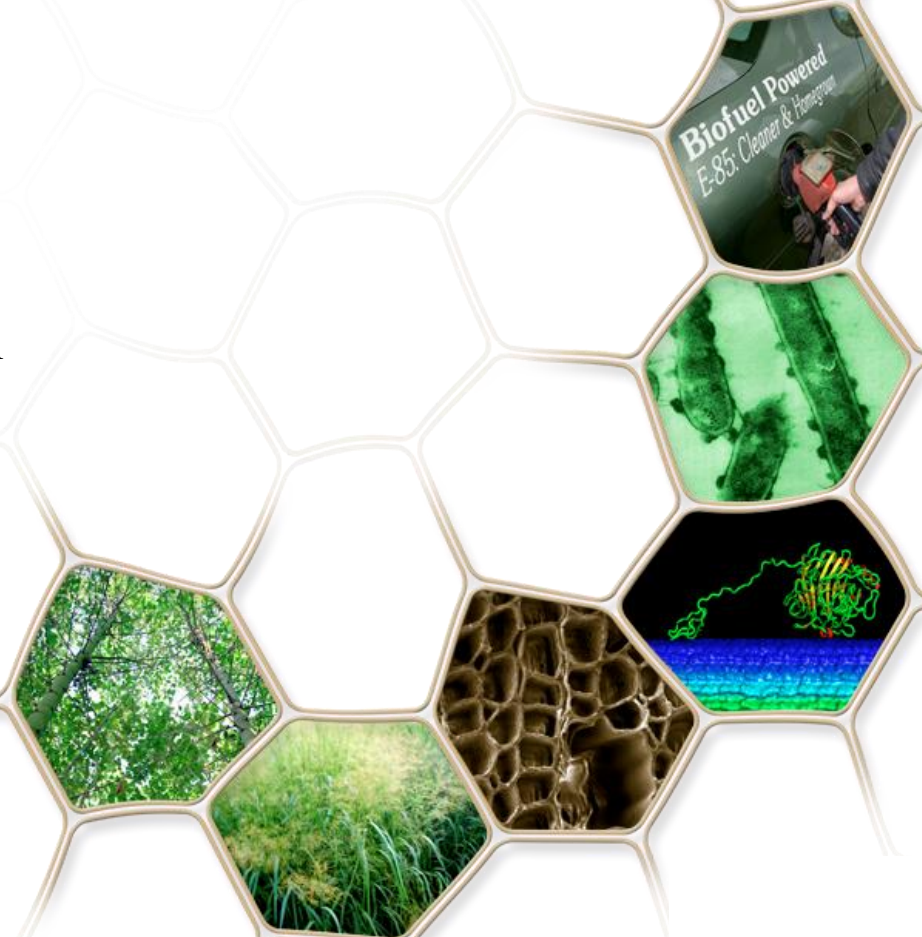
Overview and Content of the Talk

- Carbon Allocation and Partitioning

- QTL Analyses
  - Carbon allocation
  - Carbon Partitioning

- GWAS Analyses
  - Aboveground Carbon Partitioning

- Host-driven Microbiome

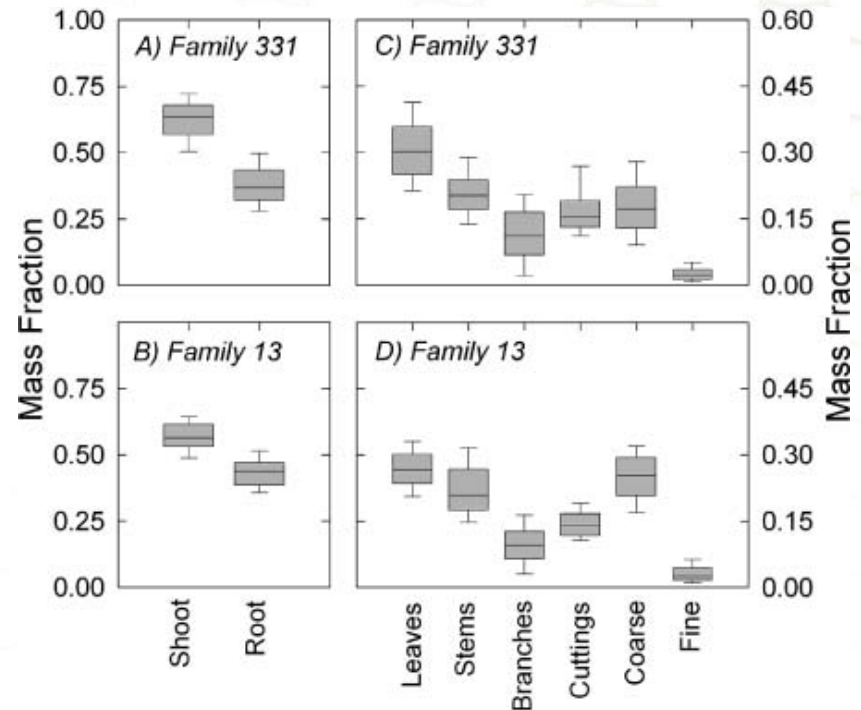**Wallula QTL planting 1st year**

Wallula QTL planting 2nd year

Carbon Allocation Above and Below Ground

- We destructively sampled two *Populus* pedigrees and segregated biomass into leaves, branches, stems, coarse roots and fine roots

- We used a saturated genetic map containing 800 SSR marker to locate QTLs associated with each biomass component

- Several highly significant QTLs were identified and interestingly there appears to be regions of the genome that independently control above and below ground traits.
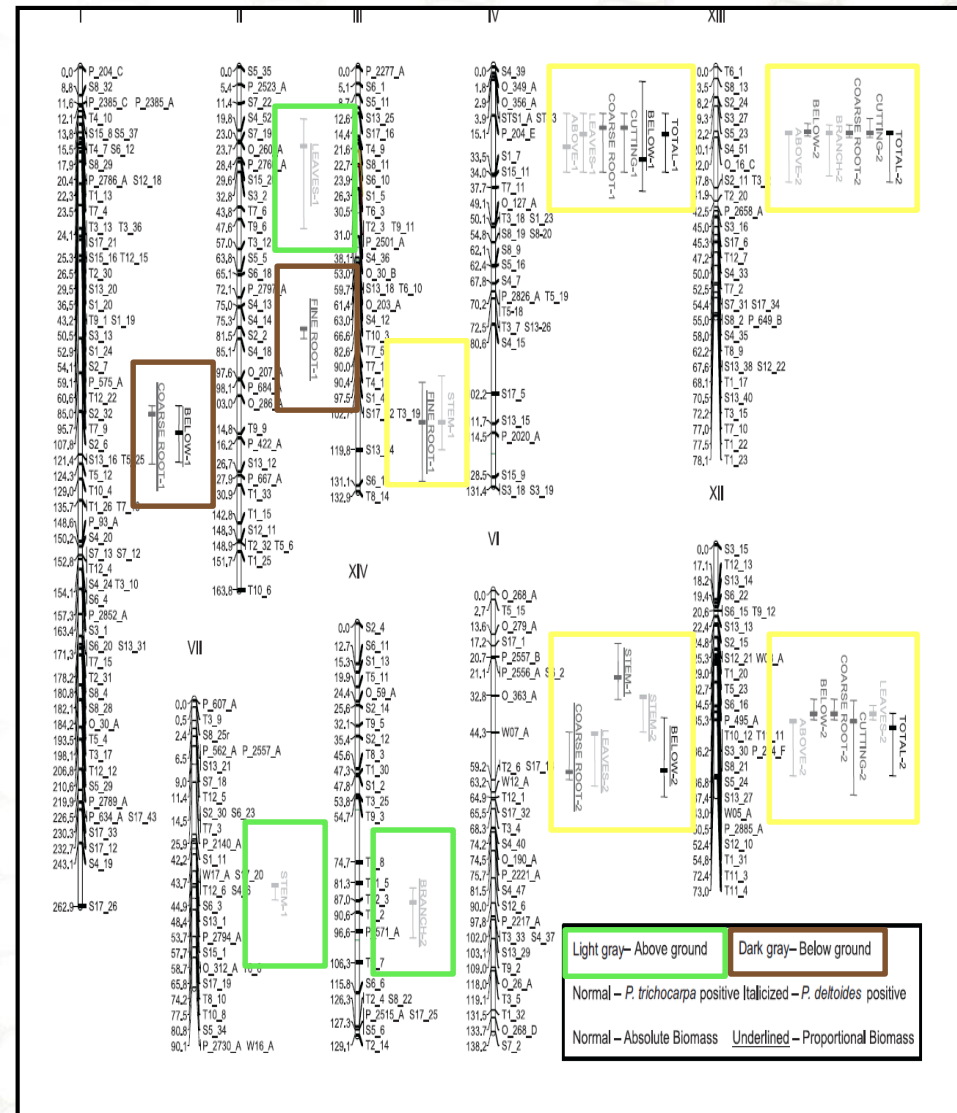
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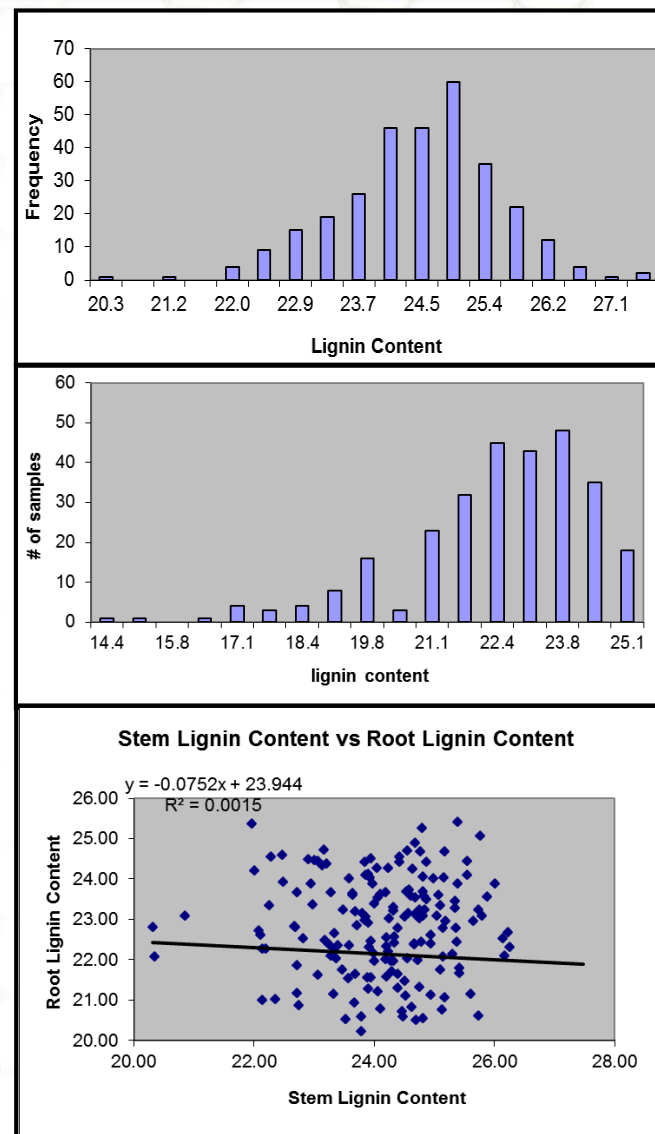

Wullschleger et al. (2005) Canadian J Forest Research 35:1779-1789.

Muchero et al. (2013) PloS ONE 8(1):e54468.

Carbon Partitioning QTL study

- We use MBMS pyrolysis to characterize cell wall chemistry in leaves, branches, stems, coarse roots and fine roots

- We again relied on the saturated genetic map containing 800 SSR marker to locate QTLs associated with each biomass component

- And again found that several highly significant QTLs were identified and interestingly there appears to be regions of the genome that independently control above and below ground traits.

Stem Lignin Content vs Root Lignin Content

$y = -0.0752x + 23.944$
$R^2 = 0.0015$

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Yin et al. (2010) PLOS ONE 5(11):e14021.

Porth et al. (2013) New Phytologist 197:777-790.
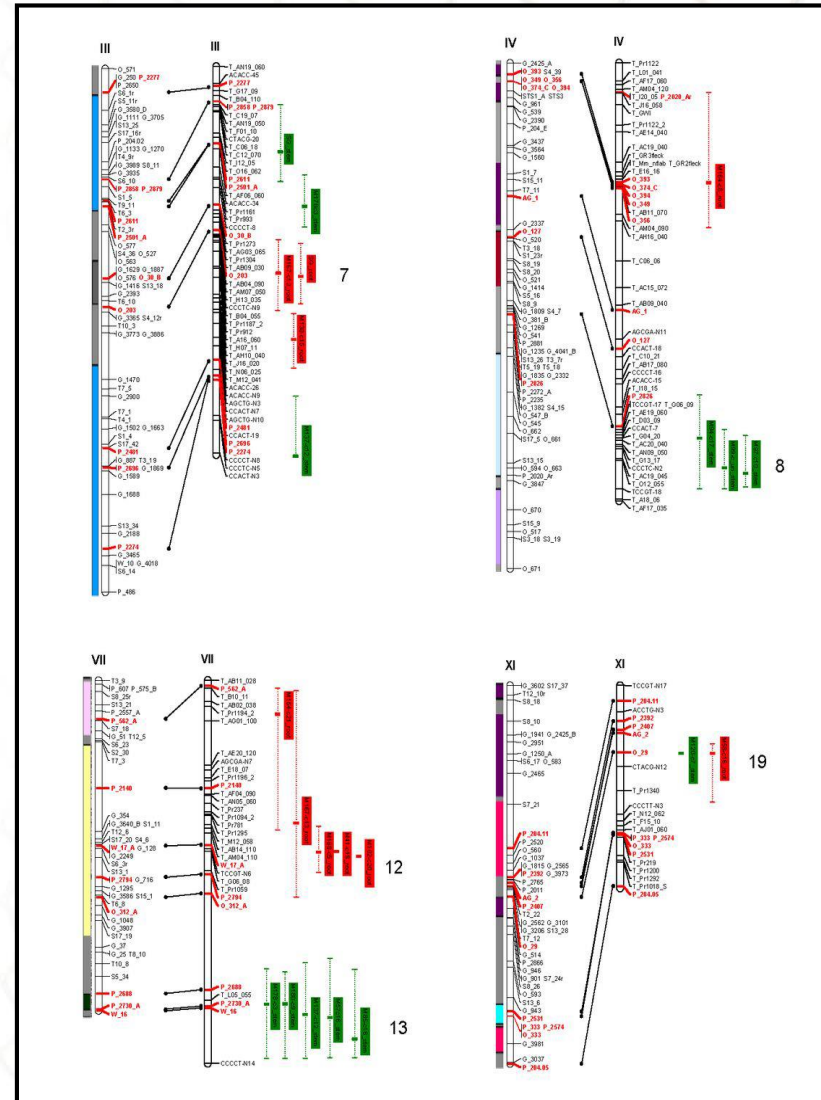
Populus Genome Released

- ***Populus* V3.0 assembly:**
  - Assembled with Arachne v20071016HA
  - Covers 423 Mb pairs out of 485 Mb total, an average read depth of 9.44X
  - Arranged in 1,446 scaffolds (2,585 gaps)
  - Integrates 81 Mb of finished sequence
  - Scaffold N50 (L50) = 8 (19.5 Mb)
  - Contig N50 (L50) = 206 (552.8 kb)
  - Represents ca. 97.3% of the genome

- ***Populus* V3.0 annotation:**
  - 75,566 RNAseq transcript assemblies
  - Constructed from 0.6 B pairs of paired-end Illumina RNAseq reads and 2.6 M 454-sequenced EST reads
  - 41,335 predicted gene models
  - 32% have splice variants
  - 73,013 total protein-coding transcripts
  - 90.5% of V2.2 loci were mapped to V3.0 loci

Tuskan et al. (2006) Science 196:726-737.

GWAS Population and SNP Detection
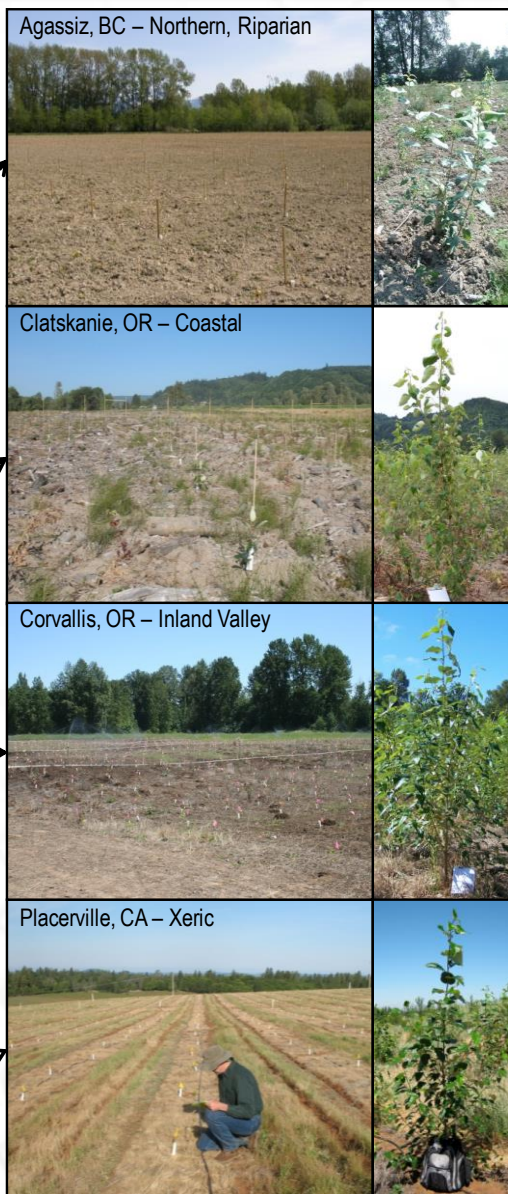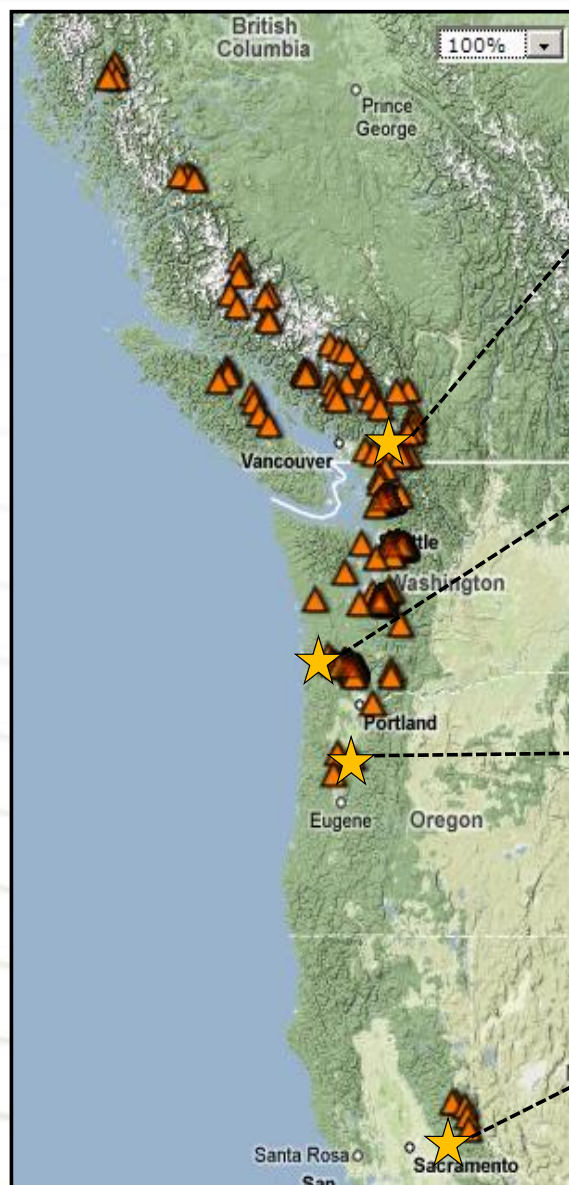
- 1084 unrelated genotypes clonally replicated in four contrasting environments

- Each genotype has been resequenced to a minimum 18X depth

- There are ca. 48 millions SNPs in the population, with a nucleotide variant every 10 bp

Slavov et al. (2012) New Phytologist 196:726-737.

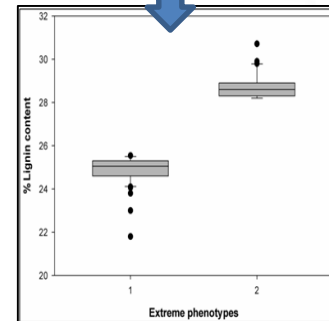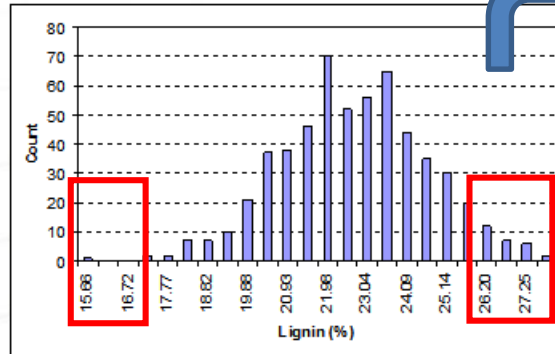**Geraldes et al. (2013) Molecular Ecology Resources In press.**

Variation in Lignin Composition and Content

Extreme variation contained in native populations of *Populus* detected in common garden experiments are linked to genes using Association Genetics
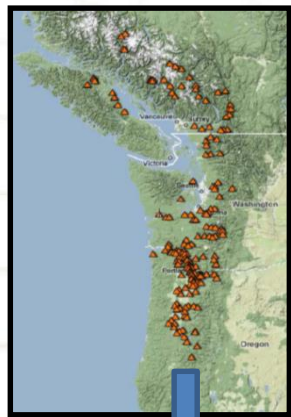
Phenotype the population

GWAS Analysis

Assemble a population

Create a SNP library
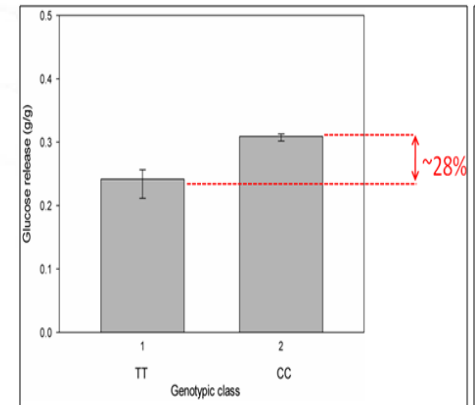
GWAS Carbon Allocation and Partitioning

- *Populus* stems vary in their roughness, from smooth to coarse

- This variation is linked to ecological function

- Populus roots also vary in this trait, and variation does not seem to be correlated

- The "corkiness" of the root bark may partially determine the rate of carbon turnover in soils
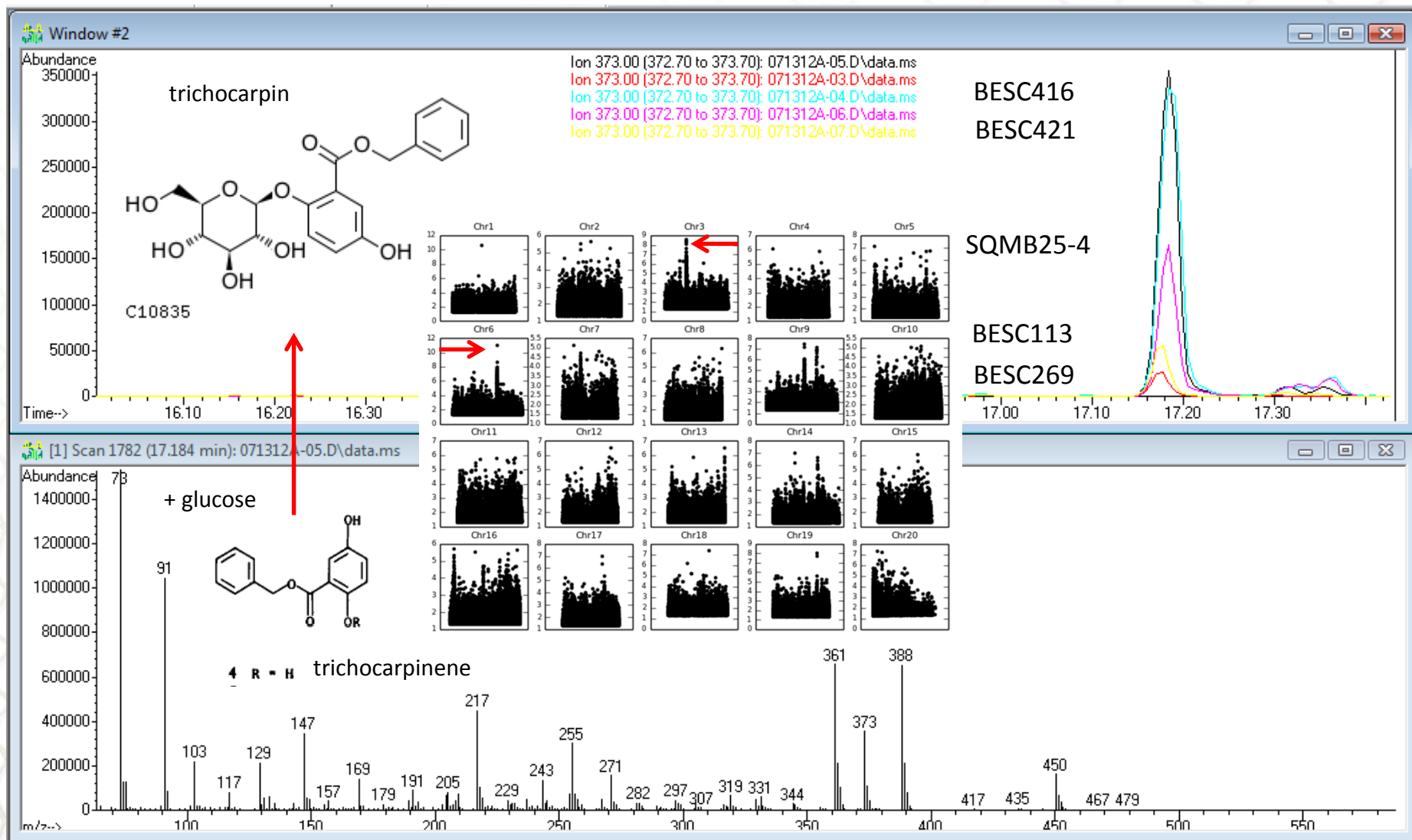
Jansson et al. (2010) BioSciences 60:685-696.

GWAS Results for Carbon Allocation

CONNEXIN: Encodes a receptor-like cytoplasmic kinase that acts as a *spatial inhibitor of cell separation*
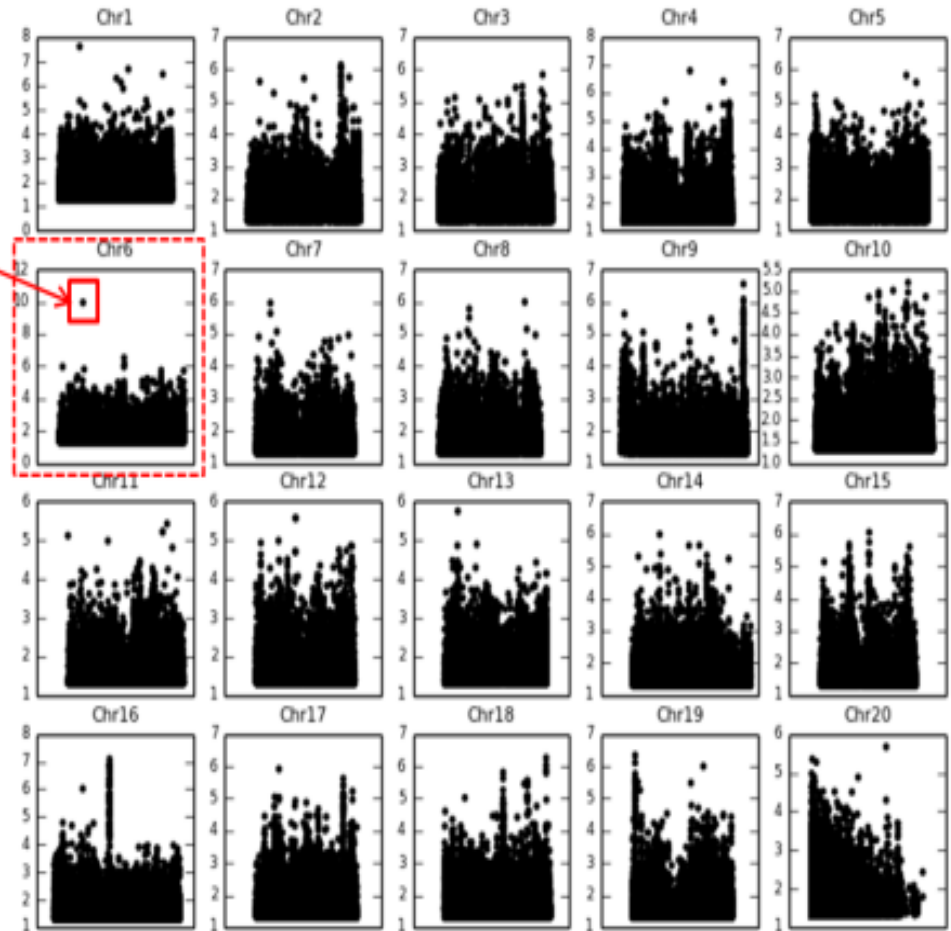
GWAS Carbon Partitioning

Chr 6 [Potri.006G171200 - UDP-glucosyl transferase 78D2] (*confirms major mQTL)
Chr 3 [Potri.003G049600 - Plant PDR ABC transporter associated]
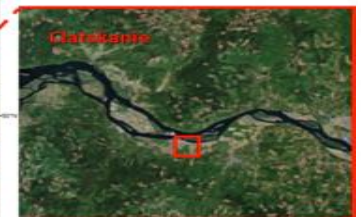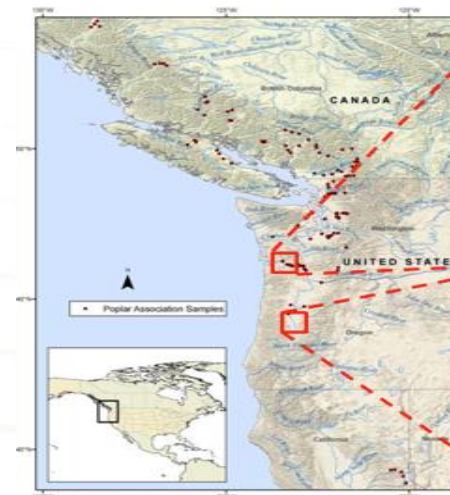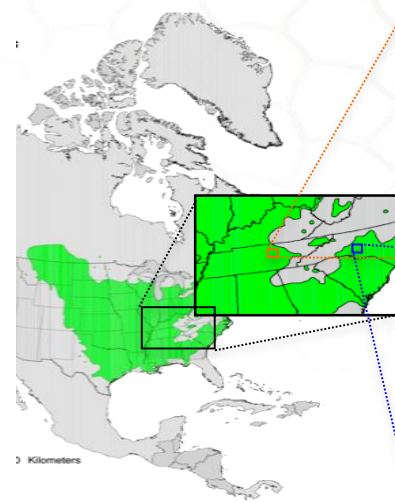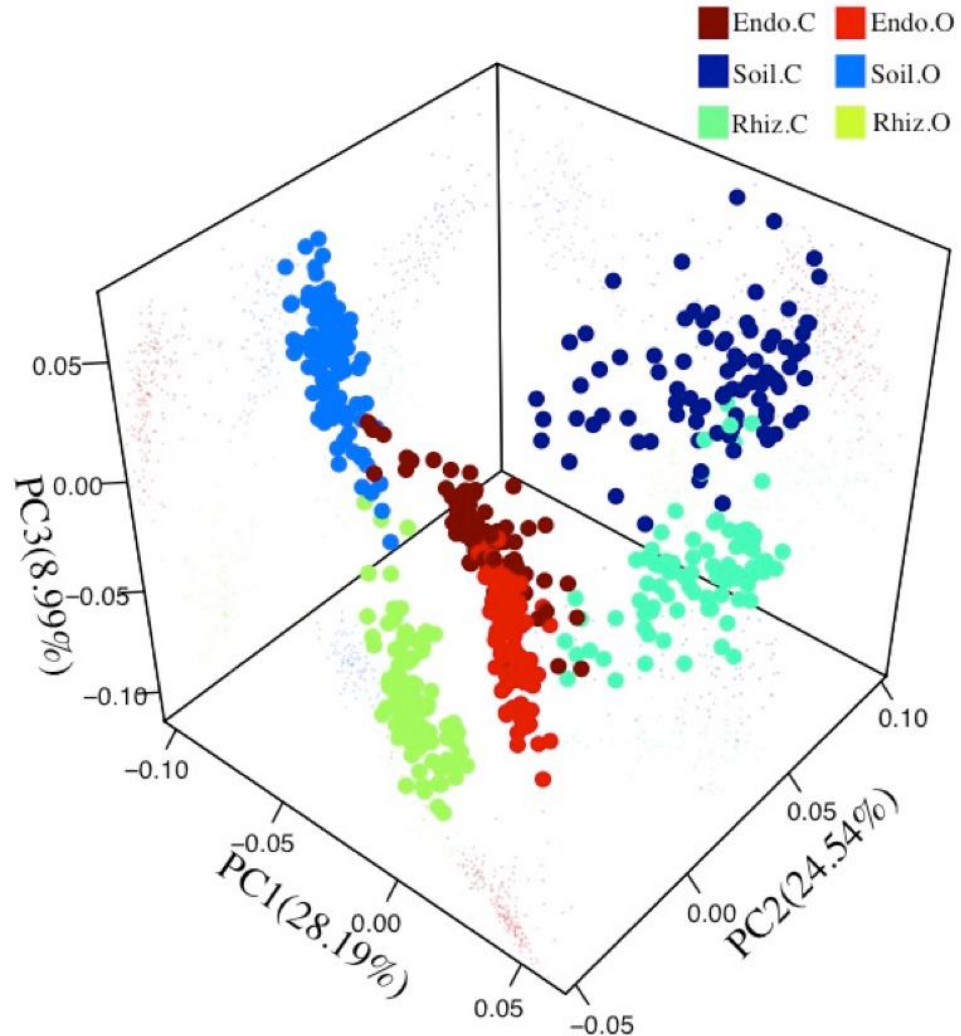
The Host Microbiome – Collection sites

13 genotypes
Caney Fork
river, TN
11 genotypes
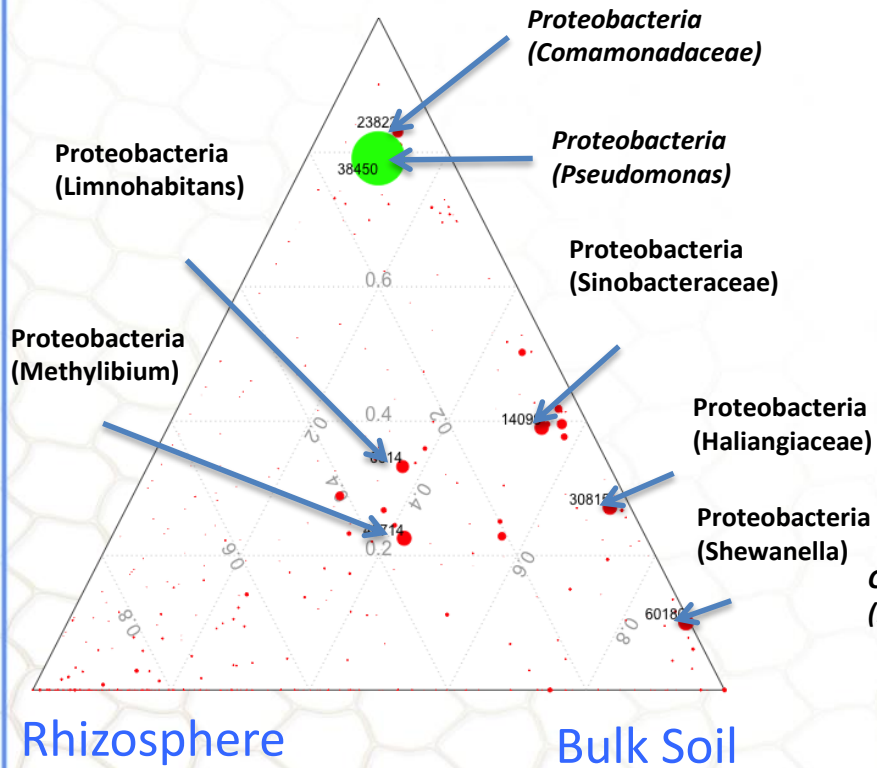Yadkin river,
NC

1087 GWAS
population at 2-
locations

The Host Microbiome – Genotype vs. Environment

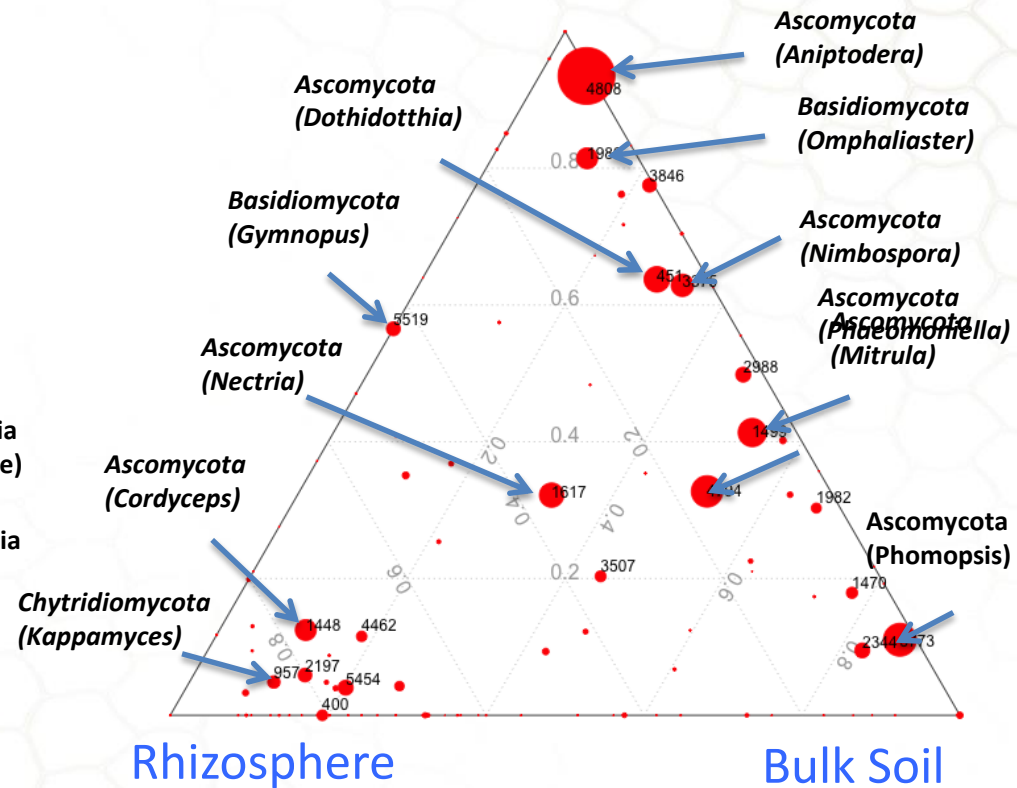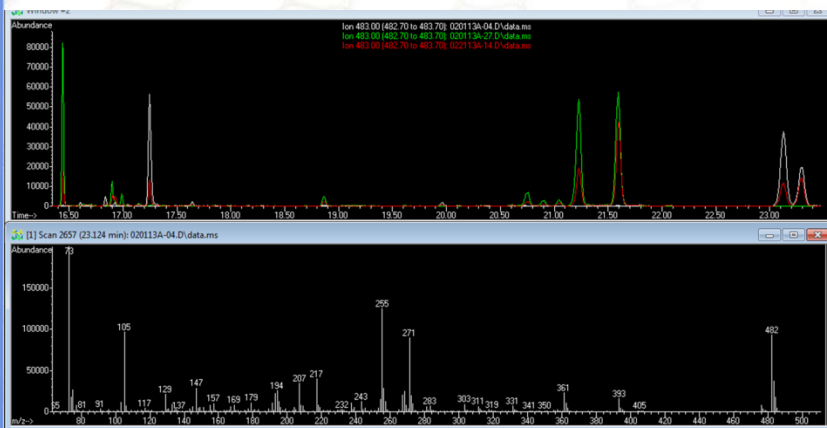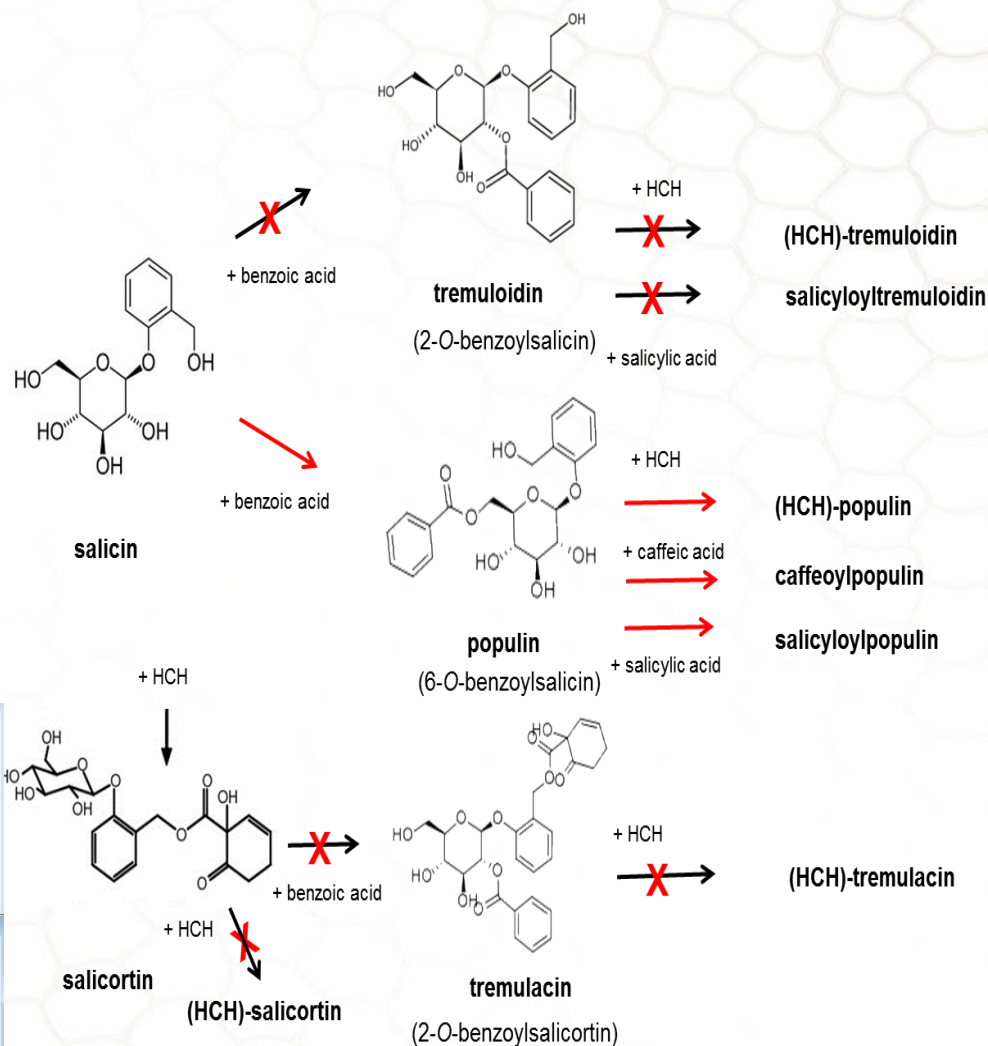# The Host Microbiome – The Microbial Atlas

Phenolic Content Impacts Endophytes

- Used broad-spectrum GC-MS profiling to identify candidate genes controlling metabolite production

- Developed an algorithm to quantify ~430 peaks

- Identified pathways can be targeted for the over-production of metabolites of interest

Summary and Conclusions

- Photosynthetic assimilation of atmospheric carbon dioxide by land plants offers the underpinnings for terrestrial carbon sequestration.

- A proportion of the C captured in plant biomass is allocated to roots, where it is partitioned into pools of soil organic C and soil inorganic C and can be sequestered for millennia.

- Carbon sequestration can be enhanced through the deliberate use of durable, engineered plant materials and the rational manipulation of the its associated microbiome